

0570  
1005

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/881,572  
Source: OIPR  
Date Processed by STIC: 7/5/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/881,572

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2   J   Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3   J   Misaligned Amino  
    Numbering           The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII           The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length       Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"                A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)         Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)         Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)         Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response            Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11   J   Use of <220>        Sequence(s)   20   missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"                Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PATENT APPLICATION 601-1-095N  
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT : Roth and Bupp  
SERIAL NO. : to be assigned  
FILED: June 14, 2001  
FOR: TARGETING VIRAL VECTORS TO SPECIFIC CELLS

STATEMENT UNDER 37 CFR §1.821 and §1.825


Commissioner for Patents  
Washington, D.C. 20231

Sir:

I hereby certify that:

X The contents of the paper Sequence Listing and computer readable Sequence Listing submitted herewith are the same. (37 CFR §1.821(f)).

Respectfully submitted,

  
\_\_\_\_\_  
Attorney for applicant(s)  
Catherine Roseman Smith  
(Reg. No. 34240)  
June 14, 2001

KLAUBER & JACKSON  
411 Hackensack Avenue  
Hackensack NJ 07601  
Tel: (201) 487-5800

Re-RUN

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/881,572

DATE: 07/05/2001

TIME: 13:31:22

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07032001\I881572.raw

Does Not Comply  
Corrected Diskette Needed

pp 1-4

QTS

3 <110> APPLICANT: Roth, Monica  
 5 Bupp, Keith.  
 7 <120> TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells  
 9 <130> FILE REFERENCE: 601-1-095N  
 11 <140> CURRENT APPLICATION NUMBER: US/09/881,572  
 12 <141> CURRENT FILING DATE: 2001-06-14  
 14 <160> NUMBER OF SEQ ID NOS: 27  
 16 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 65  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: moloney murine leukemia virus  
 23 <400> SEQUENCE: 1  
 25 His Gly Pro Ser Tyr Trp Gly Leu Glu Tyr Gln Ser Pro Phe Ser Ser  
 26 1 5 10 15  
 28 Pro Pro Gly Pro Pro Cys Cys Ser Gly Gly Ser Ser Pro Gly Cys Ser  
 29 20 25 30  
 31 Arg Asp Cys Glu Glu Pro Leu Thr Ser Leu Thr Pro Arg Cys Asn Thr  
 E--> 32 35 40 45 45  
 34 Ala Trp Asn Arg Leu Lys Leu Asp Gln Thr Thr His Lys Ser Asn Glu  
 E--> 35 50 55 60 60  
 37 Gly  
 38 65

misaligned nos.

(see item 3 on

Error Summary Sheet)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/881,572

DATE: 07/24/2001  
TIME: 09:35:17

Input Set : A:\Pto.amc  
Output Set: N:\CRF3\07242001\I881572.raw

145 <210> SEQ ID NO: 11  
146 <211> LENGTH: 6  
147 <212> TYPE: PRT  
148 <213> ORGANISM: Rat Leukemia Virus  
150 <400> SEQUENCE: 11  
152 Gly Lys Arg Thr Arg Glu  
153 1 5  
155 <210> SEQ ID NO: 12  
156 <211> LENGTH: 24  
157 <212> TYPE: PRT  
158 <213> ORGANISM: Feline Leukemia Virus  
160 <400> SEQUENCE: 12  
162 Trp Glu Pro Ile Val Leu Asp Pro Thr Asn Val Lys His Gly Ala Arg  
163 1 5 10 15  
165 Tyr Pro Ser Ser Lys Tyr Gly Cys  
166 20  
168 <210> SEQ ID NO: 13  
169 <211> LENGTH: 21  
170 <212> TYPE: PRT  
171 <213> ORGANISM: Feline Leukemia Virus  
173 <400> SEQUENCE: 13  
175 Trp Glu Pro Met Ala Pro Asp Pro Arg Ser Trp Ala Arg Tyr Ser Ser  
176 1 5 10 15  
178 Ser Ile His Gly Cys  
179 20  
181 <210> SEQ ID NO: 14  
182 <211> LENGTH: 21  
183 <212> TYPE: PRT  
OK 184 <213> ORGANISM: Artificial  
186 <220> FEATURE:  
187 <223> OTHER INFORMATION: Consensus Sequence  
189 <220> FEATURE:  
W--> 190 <221> NAME/KEY: X  
191 <222> LOCATION: (9)..(13) (10)..(14)  
192 <223> OTHER INFORMATION: (X) can be any amino acid.  
194 <220> FEATURE: Xaa  
W--> 195 <221> NAME/KEY: X  
196 <222> LOCATION: (3)..(7) (4)..(8)  
197 <223> OTHER INFORMATION: (X) is any amino acid.  
199 <400> SEQUENCE: 14 Xaa  
W--> 201 Trp Glu Pro Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Ser Ser  
202 1 5 10 15  
204 Ser Lys Tyr Gly Cys  
205 20  
207 <210> SEQ ID NO: 15  
208 <211> LENGTH: 14  
209 <212> TYPE: PRT  
210 <213> ORGANISM: Amphotropic Murine Leukemia Virus  
212 <400> SEQUENCE: 15

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/881,572

DATE: 07/24/2001  
TIME: 09:35:17

Input Set : A:\Pto.amc  
Output Set: N:\CRF3\07242001\I881572.raw

214 Glu Glu Trp Asp Pro Ser Asp Gln Glu Pro Tyr Val Gly Tyr  
215 1 5 10  
217 <210> SEQ ID NO: 16  
218 <211> LENGTH: 13  
219 <212> TYPE: PRT  
220 <213> ORGANISM: Amphotropic Murine Leukemia Virus  
222 <400> SEQUENCE: 16  
224 Pro Trp Asp Thr Gly Cys Ser Lys Val Ala Cys Gly Pro  
225 1 5 10  
227 <210> SEQ ID NO: 17  
228 <211> LENGTH: 29  
229 <212> TYPE: PRT  
230 <213> ORGANISM: Amphotropic Murine Leukemia Virus  
232 <400> SEQUENCE: 17  
234 Val Gly Asp Thr Trp Glu Pro Ile Val Leu Asn Pro Thr Asn Val Lys  
235 1 5 10 15  
237 His Gly Ala Arg Tyr Ser Ser Ser Lys Tyr Gly Cys Lys  
238 20 25  
240 <210> SEQ ID NO: 18  
241 <211> LENGTH: 26  
242 <212> TYPE: PRT  
243 <213> ORGANISM: Feline Leukemia Virus  
245 <400> SEQUENCE: 18  
247 Val Gly Thr Asp Trp Glu Pro Met Ala Pro Asp Pro Arg Ser Trp Ala  
248 1 5 10 15  
250 Arg Tyr Ser Ser Ser Thr His Gly Cys Lys  
251 20 25  
253 <210> SEQ ID NO: 19  
254 <211> LENGTH: 19  
255 <212> TYPE: PRT  
256 <213> ORGANISM: Feline Leukemia Virus  
258 <400> SEQUENCE: 19  
260 Val Gly Glu Glu Trp Asp Pro Ser Asp Gln Glu Pro Tyr Val Gly Tyr  
261 1 5 10 15  
263 Gly Cys Lys  
266 <210> SEQ ID NO: 20  
267 <211> LENGTH: 72  
268 <212> TYPE: DNA  
269 <213> ORGANISM: Artificial  
271 <220> FEATURE:  
272 <223> OTHER INFORMATION: n is any nucleotide.  
274 <220> FEATURE:  
W--> 275 <221> NAME/KEY: N  
276 <222> LOCATION: (22)..(36)  
277 <223> OTHER INFORMATION: N is any nucleotide.  
279 <220> FEATURE:  
W--> 280 <221> NAME/KEY: N  
281 <222> LOCATION: (39)..(53) (40)..(54)  
282 <223> OTHER INFORMATION: N is any nucleotide.

Ok> *See item 11 on Enr Summary Sheet*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/881,572

DATE: 07/24/2001  
TIME: 09:35:17

Input Set : A:\Pto.amc  
Output Set: N:\CRF3\07242001\I881572.raw

284 <400> SEQUENCE: 20  
W--> 285 gtgggagaca cctgggaacc tnnnnnnnnnn nnnnnnnagan nnnnnnnnnnn nnnnnnnnnnn 60  
287 tcaaaatgat ga 72  
290 <210> SEQ ID NO: 21  
291 <211> LENGTH: 17  
292 <212> TYPE: DNA  
293 <213> ORGANISM: Feline Leukemia Virus  
295 <400> SEQUENCE: 21  
296 ctctgtggac ccttgga 17  
299 <210> SEQ ID NO: 22  
300 <211> LENGTH: 22  
301 <212> TYPE: DNA  
302 <213> ORGANISM: Feline Leukemia Virus  
304 <400> SEQUENCE: 22  
305 aggaggagtt ttatacctac at 22  
308 <210> SEQ ID NO: 23  
309 <211> LENGTH: 25  
310 <212> TYPE: PRT  
311 <213> ORGANISM: Homo sapiens  
W--> 312 <220> FEATURE:  
W--> 313 <221> NAME/KEY: X  
314 <222> LOCATION: (4)..(6)  
315 <223> OTHER INFORMATION: (X) is any amino acid.  
W--> 317 <220> FEATURE:  
W--> 318 <221> NAME/KEY: X  
319 <222> LOCATION: (17)..(19)  
320 <223> OTHER INFORMATION: (X) is any amino acid.  
322 <400> SEQUENCE: 23  
W--> 324 Trp Glu Pro Xaa Xaa Xaa Ser Pro Tyr Ser Ser Asp Thr Thr Pro Ala  
325 1 5 10 15  
W--> 327 Xaa Xaa Xaa Ser Ser Lys Tyr Gly Cys  
328 20 25  
330 <210> SEQ ID NO: 24  
331 <211> LENGTH: 25  
332 <212> TYPE: PRT  
333 <213> ORGANISM: Amphotropic Murine Leukemia Virus  
335 <400> SEQUENCE: 24  
337 Glu Glu Trp Asp Pro Ser Asp Gln Glu Pro Tyr Val Gly Tyr Gly Cys  
338 1 5 10 15  
340 Lys Tyr Pro Ala Gly Arg Gln Arg Thr  
341 20 25  
343 <210> SEQ ID NO: 25  
344 <211> LENGTH: 29  
345 <212> TYPE: PRT  
346 <213> ORGANISM: Amphotropic Murine Leukemia Virus  
348 <400> SEQUENCE: 25  
350 Pro Trp Asp Thr Gly Cys Ser Lys Val Ala Cys Gly Pro Cys Tyr Asp  
351 1 5 10 15  
353 Leu Ser Lys Val Ser Asn Ser Phe Gln Gly Ala Thr Arg

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/881,572

DATE: 07/24/2001

TIME: 09:35:18

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07242001\I881572.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:184 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:190 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:269 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:312 M:283 W: Missing Blank Line separator, <220> field identifier  
L:313 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/881,572

DATE: 07/05/2001

TIME: 13:31:23

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07032001\I881572.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:32 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
 M:332 Repeated in SeqNo=1  
 L:184 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
 L:190 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
 L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
 L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
 L:269 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
 L:275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
 L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
 L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
 L:312 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:313 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
 L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
 L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
 L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23